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| FORM PTO-1449 | ATTY. DOC. NO. 245[illegible] | SERIAL NO. 09/490,702 |
|---|---|---|
| LIST OF PATENTS AND OTHER ITEMS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT | APPLICANT: Mandell, Arnold et al. | |
| (Use several sheets if necessary) | FILING DATE: January 24, 2000 | GROUP: 1643 |

PTO 09/767460 01/23/01

U.S. PATENT DOCUMENTS

| EXAMINER INITIAL | | DOCUMENT NUMBER | DATE | NAME | CLASS | SUB CLASS | FILING DATE |
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FOREIGN PATENT DOCUMENTS

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| | AB | | | | | | | |

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, etc.)

| | | |
|---|---|---|
| | AC | Mandell, A.J. (1984) Non-equilibrium behavior of some brain enzyme and receptor systems. Ann. Rev. Pharm. Toxicol. 24:237-274. |
| | AD | Mandell, A.J., Russo, P.V. and Blomgren, B.W. (1987) Complex hydrophobic sequence transformation predicts mutual recognition by polypeptides and proteins. Ann. N.Y. Acad. Sci. 504:88-118. |
| | AE | Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Mode matches and their locations in the hydrophobic free energy sequences of peptide ligands and their receptor eigenfunctions. Proc. Natl. Acad. Sci. 94:13576-13581. |
| | AF | Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Wavelet transformation of protein hydrophobicity sequences suggests their memberships in structural families. Physica A224:254-262. |
| | AG | Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Hydrophobic free energy eigenfunctions help define continuous wavelet transformations of amino acid sequences of protein families. Proc. Intl. (Fermi) Sch. Phys. CXXXIV, 175-192. |
| | AH | Di Marzo, E.A and Mandell, A.J. (1997) Phase transition behavior of a linear macromolecule threading a membrane. J. Chem. Physics 197:5510-5514. |
| | AI | Mandell, A.J., Owens, M.J., Selz, K.A., Morgan, W.N., Shlesinger, M.F. and Nemeroff, C.G. (1998) Mode matches in hydrophobic free energy eigenfunctions predict protein-protein interactions. Biopolymers 46:89-101. |
| | AJ | Selz, K.A., Mandell, A.J., and Shlesigner, M.F. (1998) Hydrophobic free energy eigenfunctions of pore, channel and transporter proteins contain β-burst patterns. Biophysical J. 7:2332-2342. |
| | AK | Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1998) Transformational homologies in amino acid sequences suggest membership in protein families. J. Stat. Phys. 93:673-697. |
| | AL | Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1999) Linear and entropic transformations of the hydrophobic free energy sequence help characterize a novel brain polyprotein: CART. In (M.T. Batchelor and L. Wille, eds.), Statistical Physics on the Eve of the Twenty-First Century, World Scientific, NJ. pp. 131-152. |
| | AM | Manavalan, P. and Ponnuswamy, P.K. (1978) Hydrophobic character of amino acid residues in globular proteins. Nature 275:673-674. |
| | AN | White, Stephen H. (1994) Global Statistics of Protein Sequences: Implications for the Origin, Evolution, and Prediction of Structure. Annu. Rev. Biophys. Biomol. Struct. 23:407-439. |
| | AO | Doyle, P.M. (1995) Combinatorial Chemistry in the Discovery and Development of Drugs. J. Chem. Tech. Biotechnol. 64:317-324. |
| | AP | Gordon, E.M., Barrett, R.W., Dower, W.J., Fodor, S.P.A. and Gallop, M.A. (1994) Applications of Combinatorial Technologies to Drug Discovery. 2. Combinatorial Organic Synthesis, Library Screening Strategies, and Future Directions. J. Med. Chem. 37(10):1385-1401. |
| | AQ | Houghton, R.A. (1993) The Broad Utility Of Soluble Peptide Libraries [illegible] |

DATE CONSIDERED

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